

We claim:

1           1.       A hGR 1Ap/e gene of the human glucocorticoid receptor promoter 1A and exon 1A  
2       comprising at least 2056 bases of SEQ ID NO: 1.

1           2.       A hGR 1Ap/e gene as in Claim 1, wherein the promoter region comprises the region  
2       from -1075 to -1 of SEQ ID NO: 1 as numbered in Figure 1.

1           3.       A hGR 1Ap/e gene as in Claim 1, wherein the exon region comprises the region from  
2       +1 to +981 of SEQ ID NO: 1 as numbered in Figure 1.

1           4.       A human glucocorticoid receptor exon 1A region as in Claim 3, wherein transcription  
2       of the exon region results in a mRNA transcript.

1           5.       A mRNA transcript of human glucocorticoid receptor exon 1A region as in Claim 4,  
2       wherein the transcript results from transcription of the region +1 to +212 of SEQ ID NO: 1 as numbered  
3       in Figure 1.

1           6.       A mRNA transcript of human glucocorticoid receptor exon 1A region as in claim 4,  
2       wherein the transcript results from transcription of the region +1 to +308 of SEQ ID NO: 1 as numbered  
3       in Figure 1.

1           7.       A mRNA transcript of human glucocorticoid receptor exon 1A region as in claim 4,  
2       wherein the transcript results from transcription of the region +1 to +981 of SEQ ID NO: 1 as numbered  
3       in Figure 1.

1           **8.**       A method to detect the presence of cancerous lymphocytes in a human, comprising  
2     assaying for the expression of the mRNA transcript as in claim 7 in human lymphocytes by using  
3     primers chosen from the sequence from +308 to +981 of SEQ ID NO: 1 as numbered in Figure 1.

1           **9.**       The method of claim 8, wherein the cancerous lymphocytes are T-cell acute  
2     lymphoblastic leukemia cells.

1           **10.**      A method to determine the responsiveness of a patient with cancerous lymphocytes to  
2     future treatment with glucocorticoids, comprising isolating lymphocytes from the patient, treating the  
3     isolated lymphocytes with glucocorticoid, and assaying for the expression of mRNA transcripts as given  
4     in Claim 7 in the treated lymphocytes using primers chosen from the sequence from +308 to +981 of  
5     SEQ ID NO: 1 as numbered in Figure 1.

1           **11.**      A method to increase the expression of mRNA as in claim 7, comprising adding an  
2     exogenous substance that causes an increased concentration of interferon regulatory factor, wherein the  
3     interferon regulatory factor binds to the DNA sequence somewhere between +102 and +125 in SEQ ID.  
4     NO. 1 as numbered in Figure 1.

1           **12.**      A method as in claim 11, wherein the exogenous substance is interferon.

1           **13.**      A method to increase the expression of mRNA transcript as in Claim 7 to treat a patient  
2     with T-cell acute lymphoblastic leukemia cells, comprising administering to the patient an enhancing  
3     amount of exogenous interferon and exogenous glucocorticoid.

1           **14.**      A method to increase the expression of mRNA transcript as in Claim 7 to treat a patient  
2     with T-cell acute lymphoblastic leukemia cells, comprising administering to the patient an enhancing  
3     amount of an exogenous demethylating agent to reactivate the human glucocorticoid promoter and exon  
4     1A activity.

- 1           **15..**     The method of claim 14, wherein the demethylating agent is 5-azacytidine.
- 1           **16.**     A hGR 1Ap/e promoter-heterologous gene construct comprising all or a portion of SEQ  
2     ID NO:1 and a heterologous gene, wherein expression of the heterologous gene of the construct is under  
3     transcriptional control of the hGR 1Ap/e promoter.
- 1           **17.**     The method of claim 16, wherein the heterologous gene codes for a toxin.
- 1           **18.**     A method to kill targeted cells by administering an exogenous dose of glucocorticoid,  
2     comprising transforming targeted cells by introducing into said cells the gene construct of claim 17.
- 1           **19.**     A method to convert glucocorticoid-resistant lymphoblasts to glucocorticoid-sensitive  
2     lymphoblasts, comprising introducing all or a functional portion of SEQ ID NO: 1 into the hormone-  
3     resistant lymphoblasts.
- 1           **20.**     An antisense transgene comprising all or a functional portion of the promoter region  
2     of SEQ ID NO: 1 linked to a fragment of the exon region of SEQ ID NO:1 in the antisense orientation.
- 1           **21.**     A method to inhibit hGR1A GR mRNA from being up-regulated in cells, comprising  
2     introducing into said cells the antisense transgene of Claim 20.
- 1           **22.**     A method to prevent neuronal apoptosis caused by excessive glucocorticoid secretion,  
2     comprising introducing into said neuronal cells the antisense transgene of Claim 20.